RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/661, 984 B _____

Source: _____ JFW16 _____

Date Processed by STIC: _____ 05/24/2006 _____

ENTERED

IFW16

RAW SEQUENCE LISTING   DATE: 05/24/2006
PATENT APPLICATION: US/10/661,984B TIME: 10:23:20

Input Set : A:\13751-056001.TXT
Output Set: N:\CRF4\05242006\J661984B.raw

```
  4 <110> APPLICANT: Sah, Dinah Wen-Yee
  5        Rossomando, Anthony
  6        Johansen, Teit E.
  8 <120> TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTORS
 10 <130> FILE REFERENCE: 13751-056001
 12 <140> CURRENT APPLICATION NUMBER: US 10/661,984B
 13 <141> CURRENT FILING DATE: 2003-09-12
 15 <150> PRIOR APPLICATION NUMBER: US 09/804,615
 16 <151> PRIOR FILING DATE: 2001-03-12
 18 <150> PRIOR APPLICATION NUMBER: PCT/EP02/02691
 19 <151> PRIOR FILING DATE: 2002-03-12
 21 <160> NUMBER OF SEQ ID NOS: 76
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 865
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Homo sapiens
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (120)...(719)
 34 <221> NAME/KEY: 5'UTR
 35 <222> LOCATION: (1)...(119)
```

W--> `37 <221> 3'UTR`
```
 38 <222> LOCATION: (720)...(865)
```
W--> `40 <221> sig_peptide`
```
 41 <222> LOCATION: (120)...(179)
```
W--> `43 <221> mat_peptide`
```
 44 <222> LOCATION: (405)...(719)
```
W--> `46 <400> 1`
```
 47 ctaggagccc atgcccggcc tgatctcagc ccgaggacag cccctccttg aggtccttcc      60
 48 tccccaagcc cacctgggtg ccctctttct ccctgaggct ccacttggtc tctccgcgc      119
 49 atg cct gcc ctg tgg ccc acc ctg gcc gct ctg gct ctg ctg agc agc      167
 50 Met Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu Leu Ser Ser
 51 -20             -15                 -10                    -5
 53 gtc gca gag gcc tcc ctg ggc tcc gcg ccc cgc agc cct gcc ccc cgc      215
 54 Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg
 55               1                 5                   10
 57 gaa ggc ccc ccg cct gtc ctg gcg tcc ccc gcc ggc cac ctg ccg ggg      263
 58 Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
 59             15                  20                  25
 61 gga cgc acg gcc cgc tgg tgc agt gga aga gcc cgg cgg ccg cgc cgc      311
 62 Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg
 63       30                  35                  40
```

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            Input Set : A:\13751-056001.TXT
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65 aga cac ttc tcg gcc cgc gcc ccc gcc gcc tgc acc ccc atc tgc tct   359
66 Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
67 45   50   55   60
69 tcc ccg cgg gtc cgc gcg gcg cgg ctg ggg ggc cgg gca gcg cgc tcg   407
70 Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
71   65   70   75
73 ggc agc ggg ggc gcg ggg tgc cgc ctg cgc tcg cag ctg gtg ccg gtg   455
74 Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
75   80   85   90
77 cgc gcg ctc ggc ctg ggc cac cgc tcc gac gag ctg gtg cgt ttc cgc   503
78 Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg
79   95   100   105
81 ttc tgc acc ggc tcc tgc ccg cgc gcg cgc tct cca cac gac ctc agc   551
82 Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser
83   110   115   120
85 ctg gcc agc cta ctg ggc gcc ggg gcc ctg cga ccg ccc ccg ggc tcc   599
86 Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
87 125   130   135   140
89 cgg ccc gtc agc cag ccc tgc tgc cga ccc acg cgc tac gaa gcg gtc   647
90 Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val
91   145   150   155
93 tcc ttc atg gac gtc aac agc acc tgg aga acc gtg gac cgc ctc tcc   695
94 Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser
95   160   165   170
97 gcc acc gcc tgc ggc tgc ctg ggc tgagggctcg ctccagggct ttgcagactg   749
98 Ala Thr Ala Cys Gly Cys Leu Gly
99   175   180
101 gacccttacc ggtggctctt cctgcctggg accctcccgc agagtcccac tagccagcgg   809
102 cctcagccag ggacgaaggc ctcaaagctg agaggcccct gccggtgggt gatgga   865
104 <210> SEQ ID NO: 2
105 <211> LENGTH: 200
106 <212> TYPE: PRT
107 <213> ORGANISM: Homo sapiens
109 <220> FEATURE:
110 <221> NAME/KEY: SIGNAL
111 <222> LOCATION: (1)...(20)
113 <400> SEQUENCE: 2
114 Met Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu Leu Ser Ser
115 -20   -15   -10   -5
116 Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg
117   1   5   10
118 Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
119   15   20   25
120 Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg
121   30   35   40
122 Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
123 45   50   55   60
124 Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
125   65   70   75

```
126 Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
127             80              85              90
128 Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg
129         95              100             105
130 Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser
131     110             115             120
132 Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
133 125             130             135             140
134 Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val
135             145             150             155
136 Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser
137         160             165             170
138 Ala Thr Ala Cys Gly Cys Leu Gly
139         175             180
141 <210> SEQ ID NO: 3
142 <211> LENGTH: 861
143 <212> TYPE: DNA
144 <213> ORGANISM: Homo sapiens
146 <220> FEATURE:
147 <221> NAME/KEY: CDS
148 <222> LOCATION: (7)...(717)
150 <221> NAME/KEY: 5'UTR
151 <222> LOCATION: (1)...(6)
W--> 153 <221> 3'UTR
154 <222> LOCATION: (718)...(861)
W--> 156 <221> sig_peptide
157 <222> LOCATION: (7)...(174)
W--> 159 <221> mat_peptide
160 <222> LOCATION: (298)...(717)
W--> 162 <221> mat_peptide
163 <222> LOCATION: (370)...(717)
W--> 165 <221> mat_peptide
166 <222> LOCATION: (379)...(717)
W--> 168 <400> 3
169 gagccc atg ccc ggc ctg atc tca gcc cga gga cag ccc ctc ctt gag        48
170        Met Pro Gly Leu Ile Ser Ala Arg Gly Gln Pro Leu Leu Glu
171        -55             -50             -45
173 gtc ctt cct ccc caa gcc cac ctg ggt gcc ctc ttt ctc cct gag gct       96
174 Val Leu Pro Pro Gln Ala His Leu Gly Ala Leu Phe Leu Pro Glu Ala
175         -40             -35             -30
177 cca ctt ggt ctc tcc gcg cag cct gcc ctg tgg ccc acc ctg gcc gct      144
178 Pro Leu Gly Leu Ser Ala Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala
179     -25             -20             -15
181 ctg gct ctg ctg agc agc gtc gca gag gcc tcc ctg ggc tcc gcg ccc      192
182 Leu Ala Leu Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro
183 -10             -5              1               5
185 cgc agc cct gcc ccc cgc gaa ggc ccc ccg cct gtc ctg gcg tcc ccc      240
186 Arg Ser Pro Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro
187         10              15              20
```

RAW SEQUENCE LISTING   DATE: 05/24/2006
PATENT APPLICATION: US/10/661,984B   TIME: 10:23:20

Input Set : A:\13751-056001.TXT
Output Set: N:\CRF4\05242006\J661984B.raw

```
189 gcc ggc cac ctg ccg ggg gga cgc acg gcc cgc tgg tgc agt gga aga     288
190 Ala Gly His Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg
191         25                  30                  35
193 gcc cgg cgg ccg ccg ccg cag cct tct cgg ccc gcg ccc ccg ccg cct     336
194 Ala Arg Arg Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro
195     40                  45                  50
197 gca ccc cca tct gct ctt ccc cgc ggg ggc cgc gcg gcg cgg gct ggg     384
198 Ala Pro Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly
199 55                  60                  65                  70
201 ggc ccg ggc aac cgc gct cgg gca gcg ggg gcg cgg ggc tgc cgc ctg     432
202 Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu
203                 75                  80                  85
205 cgc tcg cag ctg gtg ccg gtg cgc gcg ctc ggc ctg ggc cac cgc tcc     480
206 Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser
207                 90                  95                 100
209 gac gag ctg gtg cgt ttc cgc ttc tgc agc ggc tcc tgc cgc cgc gcg     528
210 Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala
211         105                 110                 115
213 cgc tct cca cac gac ctc agc ctg gcc agc cta ctg ggc gcc ggg gcc     576
214 Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala
215     120                 125                 130
217 ctg cga ccg ccc ccg ggc tcc cgg ccc gtc agc cag ccc tgc tgc cga     624
218 Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg
219 135                 140                 145                 150
221 ccc acg cgc tac gaa gcg gtc tcc ttc atg gac gtc aac agc acc tgg     672
222 Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp
223                 155                 160                 165
225 aga acc gtg gac cgc ctc tcc gcc aac ccc tgc ggc tgc ctg ggc         717
226 Arg Thr Val Asp Arg Leu Ser Ala Asn Pro Cys Gly Cys Leu Gly
227             170                 175                 180
229 tgagggctcg ctccagggct ttgcagactg gacccttacc ggtggctctt cctgcctggg   777
230 accctcccgc agagtcccac tagccagcgg cctcagccag ggacgaaggc ctcaaagctg   837
231 agaggcccct gccggtgggt gatg                                          861
```

233 <210> SEQ ID NO: 4
234 <211> LENGTH: 237
235 <212> TYPE: PRT
236 <213> ORGANISM: Homo sapiens
238 <220> FEATURE:
239 <221> NAME/KEY: SIGNAL
240 <222> LOCATION: (1)...(56)
242 <400> SEQUENCE: 4

```
243 Met Pro Gly Leu Ile Ser Ala Arg Gly Gln Pro Leu Leu Glu Val Leu
244     -55                 -50                 -45
245 Pro Pro Gln Ala His Leu Gly Ala Leu Phe Leu Pro Glu Ala Pro Leu
246 -40                 -35                 -30                 -25
247 Gly Leu Ser Ala Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala
248                 -20                 -15                 -10
249 Leu Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser
250             -5                   1                   5
```

```
251 Pro Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly
252     10                  15              20
253 His Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg
254 25                  30              35                  40
255 Arg Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Ala Pro
256             45              50              55
257 Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro
258             60              65              70
259 Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser
260         75              80              85
261 Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu
262     90                  95              100
263 Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser
264 105                 110             115                 120
265 Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg
266                 125             130             135
267 Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr
268             140             145             150
269 Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr
270         155             160             165
271 Val Asp Arg Leu Ser Ala Asn Pro Cys Gly Cys Leu Gly
272     170             175             180
274 <210> SEQ ID NO: 5
275 <211> LENGTH: 140
276 <212> TYPE: PRT
277 <213> ORGANISM: Homo sapiens
279 <220> FEATURE:
280 <221> NAME/KEY: VARIANT
281 <222> LOCATION: 134
282 <223> OTHER INFORMATION: Xaa = Asn or Thr
284 <221> NAME/KEY: VARIANT
285 <222> LOCATION: 135
286 <223> OTHER INFORMATION: Xaa = Ala or Pro
W--> 288 <400> 5
289 Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Ala Pro Pro
290 1                   5               10                  15
291 Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly
292             20              25              30
293 Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
294         35              40              45
295 Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
296     50                  55              60
297 Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
298 65                  70              75                  80
299 His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
300                 85              90                  95
301 Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
302                 100             105             110
303 Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/24/2006
PATENT APPLICATION: US/10/661,984B   TIME: 10:23:21

    Input Set : A:\13751-056001.TXT
    Output Set: N:\CRF4\05242006\J661984B.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 134,135
Seq#:6; Xaa Pos. 110,111
Seq#:7; Xaa Pos. 107,108
Seq#:27; N Pos. 1
Seq#:76; Xaa Pos. 5,6,7,8,9,10,11,12,15,21,22,23,24,25,26,27,28,29,30,31,32
Seq#:76; Xaa Pos. 33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51
Seq#:76; Xaa Pos. 53,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75
Seq#:76; Xaa Pos. 76,77,78,79,82,83

VERIFICATION SUMMARY   DATE: 05/24/2006
PATENT APPLICATION: **US/10/661,984B**   TIME: 10:23:21

Input Set : **A:\13751-056001.TXT**
Output Set: **N:\CRF4\05242006\J661984B.raw**

```
L:37 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:40 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:43 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:46 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:153 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:156 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:159 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:162 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:165 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:168 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:288 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:128
L:322 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:96
L:354 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:96
L:384 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:387 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:390 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:393 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:396 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:399 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:477 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:861 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:865 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:27
L:866 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
L:1749 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1753 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:76
L:1757 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:76
L:1758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:0
M:341 Repeated in SeqNo=76
```